Abstract of the Disclosure

The invention is directed to a method for the multidimensional analysis of a proteome. The method is used in biochemistry, biotechnology, medicine and in the pharmaceutical industry for purposes including diagnostics and the development of biologically active substances. It is the object of the invention to improve and facilitate quantification and identification of the proteins of a proteome and to make it possible for certain proteins to be quantified and identified for the first time. According to the invention, the proteins of the proteome are subjected to a number n of different separating processes under standardized conditions in such a way that each of the liquid fractions m1 m_1 obtained in a separating step supplies m2 m_2 liquid fractions in a subsequent separating step, wherein, after n separating steps, there are $\text{m1} * \text{m2} * ... \text{mn} = \text{M}$ $m_1 * m_2 * ... m_n = M$ liquid fractions which are identified by τ different analysis processes qualitatively and/or quantitatively by identification processes, known per se, and determined quantitatively by quantification processes which are likewise known per se, so that, after combining the analysis data in a database, an n-dimensional image of the proteome is obtained which is characterized by identifiers and quantifiers and by the position in the n-dimensional data network.